



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/901,484

Source: O1PE

Date Processed by STIC: 10/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker is available now to check sequence listings in Computer Readable Form.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>07/9214184</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n'	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/901,484

DATE: 10/23/2001
TIME: 16:31:00

Input Set : A:\GEN-T111XC3D2-seqlist.txt
Output Set: N:\CRF3\10232001\I901484.raw

3 <110> APPLICANT: Cohen, Daniel
4 Blumenfeld, Marta
5 Ilya, Chumakov
6 Bougueret, Lydie
8 <120> TITLE OF INVENTION: PROSTATE CANCER GENE
10 <130> FILE REFERENCE: GEN-T111XC3D2
12 <140> CURRENT APPLICATION NUMBER: 09/901,484
13 <141> CURRENT FILING DATE: 2001-07-09
15 <150> PRIOR APPLICATION NUMBER: 08/996,306
16 <151> PRIOR FILING DATE: 1997-12-22
18 <150> PRIOR APPLICATION NUMBER: 60/099,658
19 <151> PRIOR FILING DATE: 1998-09-09
21 <150> PRIOR APPLICATION NUMBER: 09/218,207
22 <151> PRIOR FILING DATE: 1998-12-22
24 <150> PRIOR APPLICATION NUMBER: 09/338,907
25 <151> PRIOR FILING DATE: 1999-06-23
27 <150> PRIOR APPLICATION NUMBER: 09/853,526
28 <151> PRIOR FILING DATE: 2001-05-11
30 <160> NUMBER OF SEQ ID NOS: 578
32 <170> SOFTWARE: Patent.pm

ERRORED SEQUENCES

2650 <210> SEQ ID NO: 69
 2651 <211> LENGTH: 5226
 2652 <212> TYPE: DNA
 2653 <213> ORGANISM: Homo sapiens *P4*
 2655 <400> SEQUENCE: 69
 2656 ctgtgtcccc tgggtgttcca cacqtaactcc atg cgc tac ctg ctg ccc agc gtc 54
 2657 Met Arg Tyr Leu Leu Pro Ser Val
 2658 1 5
 2659 gtg ctc ctg ggc acg qcg ccc acc tac qtg ttg gcc tgg ggg qtc tgg 102
 2660 Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp
 2661 10 15 20
 2662 cgg ctg ctc tcc gcc ttc ctg ccc gcc cgc ttc tac caa gcg ctg gac 150
 2663 Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp
 2664 25 30 35 40
 2665 gac cgg ctc tac tgc gtc tac caq agc atg gtg ctc ttc ttc gag 198
 2666 Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu
 2667 45 50 55
 2668 60 65 70 75 80 85

RAW SEQUENCE LISTING

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2674 att gtt gct gac atc ttg gcc atc agg cag aat gcg cta gga cat gtg	342
2675 Ile Val Ala Asp Ile Leu Ala Ile Arg Gln Asn Ala Leu Gly His Val	
2676 90 95 100	
2677 cgc tac gtg ctg aaa gaa ggg tta aaa tgg ctg cca ttg tat ggg tgt	390
2678 Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu Tyr Gly Cys	
2679 105 110 115 120	
2680 tac ttt gct cag cat gga gga atc tat gta aag cgc agt gcc aaa ttt	438
2681 Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe	
2682 125 130 135	
2683 aac gag aaa gag atg cga aac aag ttg cag agc tac gtg gac gca gga	486
2684 Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly	
2685 140 145 150	
2686 act cca atg tat ctt gtg att ttt cca gaa ggt aca agg tat aat cca	534
2687 Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro	
2688 155 160 165	
2689 gag caa aca aaa gtc ctt tca gct agt cag gca ttt gct gcc caa cgt	582
2690 Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg	
2691 170 175 180	
2692 ggc ctt gca gta tta aaa cat gtg cta aca cca cga ata aag gca act	630
2693 Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr	
2694 185 190 195 200	
2695 cac gtt gct ttt gat tgc atg aag aat tat tta gat gca att tat gat	678
2696 His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp	
2697 205 210 215	
2698 gtt acg gtg gtt tat gaa ggg aaa gac gat gga ggg tag cgaagagagt	727
2699 Val Thr Val Val Tyr Glu Gly Lys Asp Asp Gly Gly *	
2700 220 225	
2701 caccgaccat gacgaaattt ctctgcaaag aatgtccaaa aattcatatt cacattgatc	787
2702 gtatcgacaa aaaagatgtc ccagaagaac aagaacatat gagaagatgg ctgcatgaac	847
2703 gtttcgaaat caaagataag atgcttataag aattttatga gtcaccagat ccagaaagaa	907
2704 gaaaaagatt tcctggaaa agtgttaatt ccaaattaag tatcaagaag actttaccat	967
2705 caatgttgat cttaagtggc ttgactgcag gcatgcttat gaccgatgct ggaaggaage	1027
2706 tttatgtgaa cacctggata tatggAACCC tacttggctg cctgtgggtt actattaaag	1087
2707 catagacaag tagctgtctc cagacagtgg gatgtctac attgtctatt tttggcggtc	1147
2708 qcacatgaca tcaaattgtt tcctgaattt attaaggagt gtaaataaag ctttgttat	1207
2709 tqaagattqq ataataqaat ttgtgacgaa aqctqatatg caatggtett qqqcaaacat	1267
2710 acctqgttqt acaactttaq catcqggqct gctqgaaggq taaaqctaa atqgqatttc	1327
2711 tcctgtctq tccatttcct atqaaactaat gacaacttga qaaggctgg aggattgtgt	1387
2712 attttgcqaq tcagaatggct qcatttttga gcattaattt gcagcgtatt tcacttttc	1447
2713 tgttattttc aatttattac aacttgacag ctccaagtc ttattactaa agtatttagt	1507
2714 atcttgccagc tagttaatat ttcattttt gcttattttc acaagtcaagt gaaataaatt	1567
2715 gtatTTAGGA agtgtcagga tgTTCAAAGG aaagggtaaa aagtgttcat gggaaaaaag	1627
2716 ctctgtttag cacatgattt tattgtattt cgatttttgc tgatTTTACT catttttat	1687
2717 ttqcaaaata aatttctaatttatttqaa attqcttaat ttgcacaccc tgcacacaca	1747
2718 gaaaatggta taaaatatga qaacgaaqtt taaaattgtg actctgttattatagcaq	1807
2719 aactttaaat ttccccaaqtttttqaaqatt taqctacqc tatttagtact tccctttgtc	1867

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Input Set : A:\GEN-T111XC3D2-seqlist.txt
Output Set: N:\CRF3\10232001\I901484.raw

2723	tcacagaata	ttcattcaga	agtgcgttt	ctgttgtgtg	gtggattccc	actgggctct	2107
2724	ggtccttccc	ttggatcccg	tcagtggtc	tgcgcagcgg	cttgcacgta	gacttgcgtag	2167
2725	gaagaaatgc	agagccagcc	tgtgctgcc	actttcagag	ttgaactctt	taagcccttg	2227
2726	tgagtgggt	tcaccagcta	ctgcagaggc	atttgcatt	tgtctgtgtc	aagaagttca	2287
2727	ccttctcaag	ccagtgaaat	acagactaa	ttcgcatga	ctgaacgaat	ttgtttattt	2347
2728	cccatttagt	ttatggagc	tacacatcaa	tatgtatcgc	cttagagcaa	gagctgtgtt	2407
2729	ccaggaacca	gatcacgatt	tttagccatg	gaacaatata	tcccatggga	gaagaccttt	2467
2730	cagtgtgaac	tgttctattt	ttgtgttata	atttaaactt	cgatttcctc	atagtccttt	2527
2731	aagttgacat	ttctgtttac	tgctactgga	tttttgcgc	agaaatatat	cagtggccca	2587
2732	cattaaacat	accagttgga	tcatgataag	caaaatgaaa	qaataatqta	ttaagggaaa	2647
2733	attaagtgac	tgtgttacac	tgcttctccc	atgccagaga	ataaaacttt	tcaagcatca	2707
2734	tctttgaaga	gtcggtgtgt	gtgaatttgg	ttgtgttacat	tagaatgtat	gcacacatcc	2767
2735	atggacactc	aggatatagt	tggcctaata	atcgccccat	gggtaaaact	tatgaaaatt	2827
2736	tcctcatgt	gaattgtat	tttctcttac	ctgtaaagta	aaattttagat	caattccatg	2887
2737	tctttgttaa	gtaoagggat	ttaatataatt	ttgaatataa	tgggtatgtt	ctaaatttqta	2947
2738	actttgagag	gcaatactgt	tgaaattatg	tggattctaa	ctcattttaa	caaggtagcc	3007
2739	tgacctgcat	aagatcaactt	gaatgtttag	tttcatagaa	ctataactaat	cttctcacaa	3067
2740	aaggctata	aaatacagtc	gttgaaaaaa	atttgttac	aaaatgtttg	gaaaattttaga	3127
2741	agcttctct	taacactgtat	tgataactgac	ttgaattattt	ttctaaaattt	aagagccgta	3187
2742	tacctacctg	taagtctttt	cacatatcat	ttaaactttt	gtttgttata	ttactgttatt	3247
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2745	aatggctgt	ctgttaaca	tttttgacc	ctaaaattca	ccaacagtt	cccagtacat	3427
2746	aaaataggtt	taatgactgg	ccctgcattt	ttcacaatat	ttttccctaa	gctttgagca	3487
2747	aagttttaaa	aaaatacact	aaaataatca	aaactgttaa	gcagttatatt	agtttggta	3547
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2756	ggaggtttag	attgcagtga	gccccatggaca	taccactgca	ctacagcata	ggttacagca	4087
2757	cqagacccca	actcttagaa	aatqaaaagg	aaatatacgaa	atataaaaatt	tgcttattat	4147
2758	agacacacaaq	taactcccaq	atatgttacca	caaaaaatgt	qaaaagagag	agaaatgtct	4207
2759	acccaaqcaq	tattttgtgt	gtataatgc	aagcgcataq	taaaataatt	ttaaccttaa	4267
2760	tttgtttta	qtatgtttta	qattqaagat	tgatgttttt	attttcttgg	caqatattcc	4327
2761	gtatctgggt	gaaagctaca	atqcaatgtc	gttgttagttt	tgcattggctt	gttttataaa	4387
2762	caagattttt	tctcccttct	tttggccag	ttttcattac	tgatgttacta	cactttttqta	4447
2763	ttaaagaact	tgtttttttt	ttatcactt	gtataattga	cattatata	agactatgtt	4507
2764	acatgcaatc	attagaatca	aaatttagtac	tttggtcaaa	atatttacaa	catccacata	4567
2765	tttgtcaat	attcatgtta	ttaactgaat	ttaaaacctt	caacttattat	gaatgtctcg	4627
2766	tctgtacaat	cgtttat	ctcagtttag	agtagctaca	actcttcgtat	actatcatca	4687
2767	atattttqaca	tcttttccaa	tttqgtatgt	aaaagtaat	ctattccctgt	agcaactggg	4747
2768	qaqtcatata	tqaggtcaaa	gacatataacc	ttqttattat	aatatgtata	ctataataat	4807

RAW SEQUENCE LISTING
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Input Set : A:\GEN-T111XC3D2-seqlist.txt
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2772 tttatatgtg aatatgtaa atatgttctg caatttata aatgttcatg tctttttta 5047
2773 aaaaaqqtgtc tatcgaaatt ctgtgtctcc agcaggcaag aatacttgac taactcttt 5107
2774 tgtctcttta tggtatatttc agaataaagt ctgacttgc ttttgagat tattgggcc 5167
E--> 2775 tcattaattc agcaataaaag gaaaatatgc atttcaaaaaa *naaaaaaaaaaaaaaa* aaaaaaaaaa 5226
16099 <210> SEQ ID NO: 578
16100 <211> LENGTH: 19
16101 <212> TYPE: DNA
16102 <213> ORGANISM: Homo Sapiens
16104 <220> FEATURE:
16105 <221> NAME/KEY: misc_feature
16106 <222> LOCATION: 1..19
16107 <223> OTHER INFORMATION: potential microsequencing oligo for 99-222-109.mis2
16109 <400> SEQUENCE: 578
16110 ctgaagaaat tcataatcgt 19
E--> 16112 *(283)*
delete

see item 9 in line summary sheet

PJF

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/901,484

DATE: 10/23/2001
TIME: 16:31:04

Input Set : A:\GEN-T111XC3D2-seqlist.txt
Output Set: N:\CRF3\10232001\I901484.raw

L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
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L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:1102 M:283 W: Missing Blank Line separator, <400> field identifier
L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:1323 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:1419 M:283 W: Missing Blank Line separator, <400> field identifier
L:1737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:2775 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:69
L:2782 M:283 W: Missing Blank Line separator, <400> field identifier
L:2819 M:283 W: Missing Blank Line separator, <400> field identifier
L:2908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:72
L:2911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:2964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:2965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:2985 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
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L:3054 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
L:3228 M:283 W: Missing Blank Line separator, <400> field identifier
L:3630 M:283 W: Missing Blank Line separator, <400> field identifier
L:3641 M:283 W: Missing Blank Line separator, <400> field identifier
L:3650 M:283 W: Missing Blank Line separator, <400> field identifier
L:3659 M:283 W: Missing Blank Line separator, <400> field identifier
L:3668 M:283 W: Missing Blank Line separator, <400> field identifier
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L:3838 M:283 W: Missing Blank Line separator, <400> field identifier
L:5482 M:283 W: Missing Blank Line separator, <400> field identifier
L:5648 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY
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Input Set : A:\GEN-T111XC3D2-seqlist.txt
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L:7869 M:283 W: Missing Blank Line separator, <400> field identifier
L:7965 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:182
L:7989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:182
L:8038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8074 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8741 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:184
L:16112 M:254 E: No. of Bases conflict, LENGTH:Input:283 Counted:19 SEQ:578